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Editorial

Ready for the deluge! Introducing the new Metabarcoding and Metagenomics (MBMG) journal

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Ready for the deluge!

"*Prepare for the deluge*" was the daunting advice given back in 2008 in light of the emerging high-throughput sequencing technologies and the challenge of analysing and interpreting the enormous amount of data generated (Marshall 2008). Before the advent of high-throughput sequencing, data generation was typically the major bottleneck in molecular life sciences. In fact, in molecular ecology and evolutionary science, most of a research project's time actually went into molecular data generation, in particular when mixed environmental samples were the subject of study. What a different world we are living in now, where millions if not billions of DNA sequences can be produced within days and for comparatively little cost! In the time of Mi-, Hi-, Next- and NovaSeqs, Min- and GridIONs, or Sequels to name just a few of the platforms available, molecular life sciences have rapidly shifted from being data-poor to data-rich disciplines. Today, biological data are pushing the boundaries, with the suggestion having been made that the phrase "astronomically large" be changed to "genomically large", given that biology is about to replace astronomy as science's main data generator (Stephens et al. 2015).

Perhaps this is the "distant future" Darwin predicted back in 1859, when "light will be thrown on the origin of [humans] and [their] history", as genome-wide data allow us to

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reconstruct past colonisation routes and even historical 'liaisons' of humans and Neanderthals through the study of ancient DNA isolated from fossil remains or sediments. Today, 'omics' technology enables us to better understand how human beings are not mere individuals, but are in fact holobionts consisting of billions of bacteria which contribute to the overall performance of *Homo sapiens*. Environmental DNA barcoding and metabarcoding analyses, examining communities ranging from the deep sea to the highest mountains, have revealed that we still lack the understanding of most of the planet's organismal diversity due to unknown and cryptic species. Not only does the new sequencing technology allow us to identify and monitor species and population diversity, but it also gives us the ability to identify and assign functional genomic properties ("traits"). This helps us to understand the role of individual species in complex environmental processes such as carbon and nitrogen cycling - and to potentially incorporate this information in emerging management plans. A key advantage is that most of these analyses are no longer restricted to large and well-funded laboratories but are available to the broader scientific community. For example, the price for generating a human genome sequence has dropped by about six orders of magnitude over the last two decades. Today, barcoding analyses and population screenings are routinely performed as part of Bachelor and Masters theses around the world.

The flood of sequence data has produced a strategic alliance of biologists and computer scientists, which has energised and invigorated the field of bioinformatics. Major software packages have been generated to facilitate data handling and analysis. However, many exciting smaller tools such as conversion scripts, visualisation routines or data storage options have also evolved. Many of these remain unknown, living as 'in-house' scripts, barely mentioned in articles, thereby never reaching the broader stage despite a value that goes beyond the narrow academic interest of the individual researcher. In fact, many would be of exceptional value to a broader scientific audience and also to industry and stakeholders. The same holds true for the laboratory side of analysis. Although much of a researcher's time is devoted to isolation of nucleic acids, primer/probe development and the optimisation of reaction conditions for a multitude of applications, efforts are often duplicated as this information has not been evaluated or made accessible to the broader community without restrictions, i.e. not being locked behind a paywall.

All this sets the stage for the new journal *Metabarcoding and Metagenomics* (MBMG). The eponymous theme of the new journal lies in the prefix *"meta"*. While *"barcoding"* and *"genomics"* provide obvious topics of MBMG submissions, we specifically encourage contributions that go beyond single-species analyses and tackle more complex natural realities, e.g. community assessments or functional inferences from environmental samples. MBMG not only complements the range of journals in the field of molecular environmental life sciences, but also stands out as a novel outlet providing several unique features designed to help researchers to prepare for, and professionally deal with, the massive "deluge" of data. For example "*Emerging Techniques*" are fast-track reviewed publication formats to allow rapid publication of novel tools. "*Monitoring Schemes*" describe how genetic tools can be integrated into practical biomonitoring programmes. "*Primer/Probe Validation*" articles set the stage for new and relevant molecular primers/probes for

application in assessments of biota from single species to whole communities. In addition to the thematic focus on environmental 'omics' studies from genes to ecosystems and novel formats, there are several features we consider as key traits of the MBMG journal:

- *Quality but not quantity*. MBMG strives to publish all research that meets rigorous scientific quality standards. Maximising its impact factor is not an explicit goal of the journal. A team of world-leading international experts serving as subject editors is already in place to supervise the peer- and community-review process. We also promote the publication of formats such as "Posters" to allow the dissemination of small research projects as well as conceptual articles highlighting important new ideas.
- *Basic AND applied research*. We explicitly aim to bridge the gap between basic and applied research. Several publication formats such as "Protocols", "Applied Studies", or "Biomonitoring Schemes" focus on providing information to end-users in the field of molecular environmental research which is important in times where policymakers are considering the implementation of novel 'omics' technology, e.g. for the monitoring of changes in biodiversity.
- *Data policy*. Researchers publishing in MBMG have to share and deposit all data used for their research. This will ensure maximum transparency and reproducibility of research.
- *Speed*. The innovative format for manuscript submission provided by the publisher Pensoft allows MBMG to publish accepted articles in final format only two days after acceptance, thereby maximising speed. For articles describing "Emerging Techniques", we even have a fast-track peer-review process at no additional cost.
- *Advanced open access and machine-readability*. Articles are published in open access and in semantic HTML, XML and PDF formats. This publication strategy enhances article dissemination, enables automated and targeted searches, and facilitates the sharing of scientific data in an appropriate way around the globe.
- *Novel peer-review and editorial processes.* This is provided via the journal publishing platform ARPHA, an end-to-end publishing solution supporting the entire lifecycle of a research article, ranging from authoring through peer-review, publication to dissemination, all within a single online collaborative environment.

Finally, these distinguishing features of MBMG are complemented by the state-of-the-art technical backbone and services of the publisher Pensoft. This allows for smooth submission-to-acceptance correspondence, maximum control for authors, and help with the design of media releases. The technical editorial staff is available seven days a week to aid authors with their submissions.

We are enthusiastic about launching the new MBMG journal and will work hard to make it a major resource for researchers dealing with high-throughput environmental data, thereby changing the perception of the data deluge as an apocalyptic flood to the idea of a new universe of limitless options. We invite you all to take advantage of this opportunity and use the platform actively by reading, disseminating and publishing with MBMG!

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References

- Marshall A (2008) Prepare for the deluge. Nat Biotechnol 26: 1099. https://doi.org/10.1038/nbt1008-1099
- Stephens ZD, Lee SY, Faghri F, Campbell RH, Zhai C, Efron MJ, Iyer R, Schatz MC, Sinha S, Robinson GE (2015) Big Data: Astronomical or Genomical? PLoS Biology 13 (7): e1002195. https://doi.org/10.1371/journal.pbio.1002195